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INTELLECTUAL PROPERTY LAW
(PATENT, BIOTECHNOLOGY, COMPUTER,
TRADEMARK & TRADE SECRET LAW)

August 21, 1997

Docket No.: D6020

The Assistant Commissioner Of Patents And Trademarks
BOX NON- PROVISIONAL PATENT APPLICATION
Washington, DC 20231

Dear Sir:

Transmitted herewith for filing is the non-provisional patent application in the:
Name of: **O'Brien, *et al.***
For: ***Novel Extracellular Serine Protease***

CLAIMS AS FILED

Fee for:	Small entity	Amount
Basic fee	**$385**	**$385**
Each independent claim in excess of 3 (0)		
Each claim excess of 20 (2)		
Multiple dependent claim		
	TOTAL FILING FEE	**$385**

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X Any additional fees under 37 CFR 1.16.
X Any application processing fees under 37 CFR 1.17.

X Small Entity Statement

A small entity statement is enclosed and its benefit under 37 CFR 1.28(a) is hereby claimed.

___ Relate Back--35 U.S.C. 120

This non-provisional application claims benefit of Provisional Serial No. filed on_____.

X Assignment

The application is assigned by the inventors to the **Board of Trustees of the University of Arkansas.** Enclosed is an Assignment Recordation Form plus $40 fee.

X Power of Attorney
X is attached.
X Address all future communications to:

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X Two photocopies of this sheet are enclosed.

Date: August 21, 1997

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NOVEL EXTRACELLULAR SERINE PROTEASE

BACKGROUND OF THE INVENTION

Field of the Invention

The present invention relates generally to the fields of cellular biology and the diagnosis of neoplastic disease. More specifically, the present invention relates to a novel extracellular serine protease termed Tumor Antigen Derived Gene-14 (TADG-14).

Description of the Related Art

Extracellular proteases have been directly associated with tumor growth, shedding of tumor cells and invasion of target organs. Individual classes of proteases are involved in, but not limited to (1) the digestion of stroma surrounding the initial tumor area, (2) the

digestion of the cellular adhesion molecules to allow dissociation of tumor cells; and (3) the invasion of the basement membrane for metastatic growth and the activation of both tumor growth factors and angiogenic factors.

The prior art is deficient in the lack of effective means of screening to identify proteases overexpressed in carcinoma. The present invention fulfills this longstanding need and desire in the art.

SUMMARY OF THE INVENTION

The present invention discloses a screening system to identify proteases overexpressed in carcinoma by examining PCR products amplified from early-stage tumors, metastatic tumors, and normal ovarian epithelium.

In one embodiment of the present invention, there is provided a DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

In another embodiment of the present invention, there is provided a vector capable of expressing the DNA of the present

invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

In yet another embodiment of the present invention, there is provided a host cell transfected with the vector of the present invention, said vector expressing a TADG-14 protein

In still yet another embodiment of the present invention, there is provided a method of detecting expression of a TADG-14 mRNA, comprising the steps of: (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

Other and further aspects, features, and advantages of the present invention will be apparent from the following description of the presently preferred embodiments of the invention given for the purpose of disclosure.

BRIEF DESCRIPTION OF THE DRAWINGS

So that the matter in which the above-recited features, advantages and objects of the invention, as well as others which will become clear, are attained and can be understood in detail, more particular descriptions of the invention briefly summarized above may be had by reference to certain embodiments thereof which are illustrated in the appended drawings. These drawings form a part of the specification. It is to be noted, however, that the appended

drawings illustrate preferred embodiments of the invention and therefore are not to be considered limiting in their scope.

Figure 1 shows a comparison of PCR products derived from normal and carcinoma cDNA as shown by staining in an agarose gel. Two distinct bands (lane 2) were present in the primer pair sense-His-antisense Asp (AS1) and multiple bands of about 500 base pairs are noted in the carcinoma lane for the sense-His antisense-Ser (AS2) primer pairs (lane 4).

Figure 2 shows a comparison of the amino acid sequence of TADG-14's catalytic domains.

Figure 3 shows the overexpression of TADG-14 in ovarian carcinomas.

Figure 4 shows the TADG-14 expression in tumors and cell lines.

Figure 5 shows the blots of TADG-14 expression in fetal, adult and ovarian carcinoma tissues.

Figure 6 shows the complete sequence of the TADG-14 transcript including the open reading frame and common domains.

Figure 7 shows the homology of TADG-14 with mouse neuropsin. There was approximately 76% identity for the open reading frame and low homology outside of the open reading frame.

Figure 8 shows the amino acid homology of TADG-14 with mouse neuropsin.

DETAILED DESCRIPTION OF THE INVENTION

As used herein, the term "cDNA" shall refer to the DNA copy of the mRNA transcript of a gene.

As used herein, the term "derived amino acid sequence" shall mean the amino acid sequence determined by reading the triplet sequence of nucleotide bases in the cDNA.

As used herein the term "screening a library" shall refer to the process of using a labeled probe to check whether, under the appropriate conditions, there is a sequence complementary to the probe present in a particular DNA library. In addition, "screening a library" could be performed by PCR.

As used herein, the term "PCR" refers to the polymerase chain reaction that is the subject of U.S. Patent Nos. 4,683,195 and 4,683,202 to Mullis, as well as other improvements now known in the art.

The TADG-14 cDNA is 1343 base pairs long (SEQ IS No: 6) and encoding for a 260 amino acid protein (SEQ IS No: 7). The availability of the TADG-14 gene opens the way for a number studies that can lead to various applications. For example, the TADG-14 gene underlies a specific human genetic disease, the cDNA can be the basis for a diagnostic predictive test.

In accordance with the present invention there may be employed conventional molecular biology, microbiology, and

recombinant DNA techniques within the skill of the art. Such techniques are explained fully in the literature. See, e.g., Maniatis, Fritsch & Sambrook, "Molecular Cloning: A Laboratory Manual (1982); "DNA Cloning: A Practical Approach," Volumes I and II (D.N. Glover ed. 1985); "Oligonucleotide Synthesis" (M.J. Gait ed. 1984); "Nucleic Acid Hybridization" [B.D. Hames & S.J. Higgins eds. (1985)]; "Transcription and Translation" [B.D. Hames & S.J. Higgins eds. (1984)]; "Animal Cell Culture" [R.I. Freshney, ed. (1986)]; "Immobilized Cells And Enzymes" [IRL Press, (1986)]; B. Perbal, "A Practical Guide To Molecular Cloning" (1984).

Therefore, if appearing herein, the following terms shall have the definitions set out below.

The amino acid described herein are preferred to be in the "L" isomeric form. However, residues in the "D" isomeric form can be substituted for any L-amino acid residue, as long as the desired functional property of immunoglobulin-binding is retained by the polypeptide. NH_2 refers to the free amino group present at the amino terminus of a polypeptide. COOH refers to the free carboxy group present at the carboxy terminus of a polypeptide. In keeping with standard polypeptide nomeclature, *J Biol. Chem.*, 243:3552-59 (1969), abbreviations for amino acid residues are shown in the following Table of Correspondence:

TABLE OF CORRESPONDENCE

SYMBOL 1-Letter	3-Letter	AMINO ACID
Y	Tyr	tyrosine
G	Gly	glycine
F	Phe	Phenylalanine
M	Met	methionine
A	Ala	alanine
S	Ser	serine
I	Ile	isoleucine
L	Leu	leucine
T	Thr	threonine
V	Val	valine
P	Pro	proline
K	Lys	lysine
H	His	histidine
Q	Gln	glutamine
E	Glu	glutamic acid
W	Trp	tryptophan
R	Arg	arginine
D	Asp	aspartic acid
N	Asn	asparagine
C	Cys	cysteine

It should be noted that all amino-acid residue sequences are represented herein by formulae whose left and right orientation is in the conventional direction of amino-terminus to carboxy-terminus. Furthermore, it should be noted that a dash at the beginning or end of an amino acid residue sequence indicates a peptide bond to a further sequence of one or more amino-acid residues. The above Table is presented to correlate the three-letter and one-letter notations which may appear alternately herein.

A "replicon" is any genetic element (e.g., plasmid, chromosome, virus) that functions as an autonomous unit of DNA replication *in vivo*; i.e., capable of replication under its own control.

A "vector" is a replicon, such as plasmid, phage or cosmid, to which another DNA segment may be attached so as to bring about the replication of the attached segment.

A "DNA molecule" refers to the polymeric form of deoxyribonucleotides (adenine, guanine, thymine, or cytosine) in its either single stranded form, or a double-stranded helix. This term refers only to the primary and secondary structure of the molecule, and does not limit it to any particular tertiary forms. Thus, this term includes double-stranded DNA found, *inter alia*, in linear DNA molecules (e.g., restriction fragments), viruses, plasmids, and chromosomes. In discussing the structure herein according to the normal convention of giving only the sequence in the 5' to 3' direction along the nontranscribed strand of DNA (i.e., the strand having a sequence homologous to the mRNA).

An "origin of replication" refers to those DNA sequences that participate in DNA synthesis.

A DNA "coding sequence" is a double-stranded DNA sequence which is transcribed and translated into a polypeptide *in vivo* when placed under the control of appropriate regulatory sequences. The boundaries of the coding sequence are determined by a start codon at the 5' (amino) terminus and a translation stop codon at the 3' (carboxyl) terminus. A coding sequence can include,

but is not limited to, prokaryotic sequences, cDNA from eukaryotic mRNA, genomic DNA sequences from eukaryotic (e.g., mammalian) DNA, and even synthetic DNA sequences. A polyadenylation signal and transcription termination sequence will usually be located 3' to the coding sequence.

Transcriptional and translational control sequences are DNA regulatory sequences, such as promoters, enhancers, polyadenylation signals, terminators, and the like, that provide for the expression of a coding sequence in a host cell.

A "promoter sequence" is a DNA regulatory region capable of binding RNA polymerase in a cell and initiating transcription of a downstream (3' direction) coding sequence. For purposes of defining the present invention, the promoter sequence is bounded at its 3' terminus by the transcription initiation site and extends upstream (5' direction) to include the minimum number of bases or elements necessary to initiate transcription at levels detectable above background. Within the promoter sequence will be found a transcription initiation site, as well as protein binding domains (consensus sequences) responsible for the binding of RNA polymerase. Eukaryotic promoters often, but not always, contain "TATA" boxes and "CAT" boxes. Prokaryotic promoters contain Shine-Dalgarno sequences in addition to the -10 and -35 consensus sequences.

An "expression control sequence" is a DNA sequence that controls and regulates the transcription and translation of another

DNA sequence. A coding sequence is "under the control" of transcriptional and translational control sequences in a cell when RNA polymerase transcribes the coding sequence into mRNA, which is then translated into the protein encoded by the coding sequence.

A "signal sequence" can be included near the coding sequence. This sequence encodes a signal peptide, N-terminal to the polypeptide, that communicates to the host cell to direct the polypeptide to the cell surface or secrete the polypeptide into the media, and this signal peptide is clipped off by the host cell before the protein leaves the cell. Signal sequences can be found associated with a variety of proteins native to prokaryotes and eukaryotes.

The term "oligonucleotide", as used herein in referring to the probe of the present invention, is defined as a molecule comprised of two or more ribonucleotides, preferably more than three. Its exact size will depend upon many factors which, in turn, depend upon the ultimate function and use of the oligonucleotide.

The term "primer" as used herein refers to an oligonucleotide, whether occurring naturally as in a purified restriction digest or produced synthetically, which is capable of acting as a point of initiation of synthesis when placed under conditions in which synthesis of a primer extension product, which is complementary to a nucleic acid strand, is induced, i.e., in the presence of nucleotides and an inducing agent such as a DNA polymerase and at a suitable temperature and pH. The primer may be either single-stranded or double-stranded and must be

sufficiently long to prime the synthesis of the desired extension product in the presence of the inducing agent. The exact length of the primer will depend upon many factors, including temperature, source of primer and use the method. For example, for diagnostic applications, depending on the complexity of the target sequence, the oligonucleotide primer typically contains 15-25 or more nucleotides, although it may contain fewer nucleotides.

The primers herein are selected to be "substantially" complementary to different strands of a particular target DNA sequence. This means that the primers must be sufficiently complementary to hybridize with their respective strands. Therefore, the primer sequence need not reflect the exact sequence of the template. For example, a non-complementary nucleotide fragment may be attached to the 5' end of the primer, with the remainder of the primer sequence being complementary to the strand. Alternatively, non-complementary bases or longer sequences can be interspersed into the primer, provided that the primer sequence has sufficient complementarity with the sequence or hybridize therewith and thereby form the template for the synthesis of the extension product.

As used herein, the terms "restriction endonucleases" and "restriction enzymes" refer to enzymes, each of which cut double-stranded DNA at or near a specific nucleotide sequence.

A cell has been "transformed" by exogenous or heterologous DNA when such DNA has been introduced inside the

cell. The transforming DNA may or may not be integrated (covalently linked) into the genome of the cell. In prokaryotes, yeast, and mammalian cells for example, the transforming DNA may be maintained on an episomal element such as a plasmid. With respect to eukaryotic cells, a stably transformed cell is one in which the transforming DNA has become integrated into a chromosome so that it is inherited by daughter cells through chromosome replication. This stability is demonstrated by the ability of the eukaryotic cell to establish cell lines or clones comprised of a population of daughter cells containing the transforming DNA. A "clone" is a population of cells derived from a single cell or ancestor by mitosis. A "cell line" is a clone of a primary cell that is capable of stable growth *in vitro* for many generations.

Two DNA sequences are "substantially homologous" when at least about 75% (preferably at least about 80%, and most preferably at least about 90% or 95%) of the nucleotides match over the defined length of the DNA sequences. Sequences that are substantially homologous can be identified by comparing the sequences using standard software available in sequence data banks, or in a Southern hybridization experiment under, for example, stringent conditions as defined for that particular system. Defining appropriate hybridization conditions is within the skill of the art. See, e.g., Maniatis et al., *supra*; DNA Cloning, Vols. I & II, *supra*; Nucleic Acid Hybridization, *supra*.

A "heterologous' region of the DNA construct is an identifiable segment of DNA within a larger DNA molecule that is not found in association with the larger molecule in nature. Thus, when the heterologous region encodes a mammalian gene, the gene will usually be flanked by DNA that does not flank the mammalian genomic DNA in the genome of the source organism. In another example, coding sequence is a construct where the coding sequence itself is not found in nature (e.g., a cDNA where the genomic coding sequence contains introns, or synthetic sequences having codons different than the native gene). Allelic variations or naturally-occurring mutational events do not give rise to a heterologous region of DNA as defined herein.

The labels most commonly employed for these studies are radioactive elements, enzymes, chemicals which fluoresce when exposed to untraviolet light, and others. A number of fluorescent materials are known and can be utilized as labels. These include, for example, fluorescein, rhodamine, auramine, Texas Red, AMCA blue and Lucifer Yellow. A particular detecting material is anti-rabbit antibody prepared in goats and conjugated with fluorescein through an isothiocyanate.

Proteins can also be labeled with a radioactive element or with an enzyme. The radioactive label can be detected by any of the currently available counting procedures. The preferred isotope may be selected from ^{3}H, ^{14}C, ^{32}P, ^{35}S, ^{36}Cl, ^{51}Cr, ^{57}Co, ^{58}Co, ^{59}Fe, ^{90}Y, ^{125}I, ^{131}I, and ^{186}Re.

Enzyme labels are likewise useful, and can be detected by any of the presently utilized colorimetric, spectrophotometric, fluorospectrophotometric, amperometric or gasometric techniques. The enzyme is conjugated to the selected particle by reaction with bridging molecules such as carbodiimides, diisocyanates, glutaraldehyde and the like. Many enzymes which can be used in these procedures are known and can be utilized. The preferred are peroxidase, β-glucuronidase, β-D-glucosidase, β-D-galactosidase, urease, glucose oxidase plus peroxidase and alkaline phosphatase. U.S. Patent Nos. 3,654,090, 3,850,752, and 4,016,043 are referred to by way of example for their disclosure of alternate labeling material and methods.

A particular assay system developed and utilized in the art is known as a receptor assay. In a receptor assay, the material to be assayed is appropriately labeled and then certain cellular test colonies are inoculated with a quantitiy of both the label after which binding studies are conducted to determine the extent to which the labeled material binds to the cell receptors. In this way, differences in affinity between materials can be ascertained.

An assay useful in the art is known as a "cis/trans" assay. Briefly, this assay employs two genetic constructs, one of which is typically a plasmid that continually expresses a particular receptor of interest when transfected into an appropriate cell line, and the second of which is a plasmid that expresses a reporter such as luciferase, under the control of a receptor/ligand complex. Thus, for

example, if it is desired to evaluate a compound as a ligand for a particular receptor, one of the plasmids would be a construct that results in expression of the receptor in the chosen cell line, while the second plasmid would possess a promoter linked to the luciferase gene in which the response element to the particular receptor is inserted. If the compound under test is an agonist for the receptor, the ligand will complex with the receptor, and the resulting complex will bind the response element and initiate transcription of the luciferase gene. The resulting chemiluminescence is then measured photometrically, and dose response curves are obtained and compared to those of known ligands. The foregoing protocol is described in detail in U.S. Patent No. 4,981,784.

As used herein, the term "host" is meant to include not only prokaryotes but also eukaryotes such as yeast, plant and animal cells. A recombinant DNA molecule or gene which encodes a human TADG-14 protein of the present invention can be used to transform a host using any of the techniques commonly known to those of ordinary skill in the art. Especially preferred is the use of a vector containing coding sequences for the gene which encodes a human TADG-14 protein of the present invention for purposes of prokaryote transformation.

Prokaryotic hosts may include *E. coli*, *S. tymphimurium*, *Serratia marcescens* and *Bacillus subtilis*. Eukaryotic hosts include yeasts such as *Pichia pastoris*, mammalian cells and insect cells.

In general, expression vectors containing promoter sequences which facilitate the efficient transcription of the inserted DNA fragment are used in connection with the host. The expression vector typically contains an origin of replication, promoter(s), terminator(s), as well as specific genes which are capable of providing phenotypic selection in transformed cells. The transformed hosts can be fermented and cultured according to means known in the art to achieve optimal cell growth.

The invention includes a substantially pure DNA encoding a TADG-14 protein, a strand of which DNA will hybridize at high stringency to a probe containing a sequence of at least 15 consecutive nucleotides of (SEQ ID NO:6). The protein encoded by the DNA of this invention may share at least 80% sequence identity (preferably 85%, more preferably 90%, and most preferably 95%) with the amino acids listed in Figure 6 (SEQ ID NO: 7). More preferably, the DNA includes the coding sequence of the nucleotides of Figure 6 (SEQ ID NO:6), or a degenerate variant of such a sequence.

The probe to which the DNA of the invention hybridizes preferably consists of a sequence of at least 20 consecutive nucleotides, more preferably 40 nucleotides, even more preferably 50 nucleotides, and most preferably 100 nucleotides or more (up to 100%) of the coding sequence of the nucleotides listed in Figure 6 (SEQ ID NO: 6) or the complement thereof. Such a probe is useful for detecting expression of TADG-14 in a human cell by a method

including the steps of (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

This invention also includes a substantially pure DNA containing a sequence of at least 15 consecutive nucleotides (preferably 20, more preferably 30, even more preferably 50, and most preferably all) of the region from nucleotides 1 to 1343 of the nucleotides listed in Figure 6 (SEQ ID NO: 6).

By "high stringency" is meant DNA hybridization and wash conditions characterized by high temperature and low salt concentration, e.g., wash conditions of 65°C at a salt concentration of approximately 0.1 x SSC, or the functional equivalent thereof. For example, high stringency conditions may include hybridization at about 42°C in the presence of about 50% formamide; a first wash at about 65°C with about 2 x SSC containing 1% SDS; followed by a second wash at about 65°C with about 0.1 x SSC.

By "substantially pure DNA" is meant DNA that is not part of a milieu in which the DNA naturally occurs, by virtue of separation (partial or total purification) of some or all of the molecules of that milieu, or by virtue of alteration of sequences that flank the claimed DNA. The term therefore includes, for example, a recombinant DNA which is incorporated into a vector, into an autonomously replicating plasmid or virus, or into the genomic DNA of a prokaryote or eukaryote; or which exists as a separate molecule (e.g., a cDNA or a genomic or cDNA fragment produced by

polymerase chain reaction (PCR) or restriction endonuclease digestion) independent of other sequences. It also includes a recombinant DNA which is part of a hybrid gene encoding additional polypeptide sequence, e.g., a fusion protein. Also included is a recombinant DNA which includes a portion of the nucleotides listed in Figure 6 (SEQ ID NO: 6) which encodes an alternative splice variant of TADG-14.

The DNA may have at least about 70% sequence identity to the coding sequence of the nucleotides listed in Figure 6 (SEQ ID NO:6), preferably at least 75% (e.g. at least 80%); and most preferably at least 90%. The identity between two sequences is a direct function of the number of matching or identical positions. When a subunit position in both of the two sequences is occupied by the same monomeric subunit, e.g., if a given position is occupied by an adenine in each of two DNA molecules, then they are identical at that position. For example, if 7 positions in a sequence 10 nucleotides in length are identical to the corresponding positions in a second 10-nucleotide sequence, then the two sequences have 70% sequence identity. The length of comparison sequences will generally be at least 50 nucleotides, preferably at least 60 nucleotides, more preferably at least 75 nucleotides, and most preferably 100 nucleotides. Sequence identity is typically measured using sequence analysis software (e.g., Sequence Analysis Software Package of the Genetics Computer Group, University of

Wisconsin Biotechnology Center, 1710 University Avenue, Madison, WI 53705).

The present invention comprises a vector comprising a DNA sequence coding for a which encodes a human TADG-14 protein and said vector is capable of replication in a host which comprises, in operable linkage: a) an origin of replication; b) a promoter; and c) a DNA sequence coding for said protein. Preferably, the vector of the present invention contains a portion of the DNA sequence shown in SEQ ID No: 6. A "vector" may be defined as a replicable nucleic acid construct, e.g., a plasmid or viral nucleic acid. Vectors may be used to amplify and/or express nucleic acid encoding TADG-14 protein. An expression vector is a replicable construct in which a nucleic acid sequence encoding a polypeptide is operably linked to suitable control sequences capable of effecting expression of the polypeptide in a cell. The need for such control sequences will vary depending upon the cell selected and the transformation method chosen. Generally, control sequences include a transcriptional promoter and/or enhancer, suitable mRNA ribosomal binding sites, and sequences which control the termination of transcription and translation. Methods which are well known to those skilled in the art can be used to construct expression vectors containing appropriate transcriptional and translational control signals. See for example, the techniques described in Sambrook et al., 1989, *Molecular Cloning: A Laboratory Manual* (2nd Ed.), Cold Spring Harbor Press, N.Y. A gene and its transcription control sequences

are defined as being "operably linked" if the transcription control sequences effectively control the transcription of the gene. Vectors of the invention include, but are not limited to, plasmid vectors and viral vectors. Preferred viral vectors of the invention are those derived from retroviruses, adenovirus, adeno-associated virus, SV40 virus, or herpes viruses.

By a "substantially pure protein" is meant a protein which has been separated from at least some of those components which naturally accompany it. Typically, the protein is substantially pure when it is at least 60%, by weight, free from the proteins and other naturally-occurring organic molecules with which it is naturally associated in vivo. Preferably, the purity of the preparation is at least 75%, more preferably at least 90%, and most preferably at least 99%, by weight. A substantially pure TADG-14 protein may be obtained, for example, by extraction from a natural source; by expression of a recombinant nucleic acid encoding an TADG-14 polypeptide; or by chemically synthesizing the protein. Purity can be measured by any appropriate method, e.g., column chromatography such as immunoaffinity chromatography using an antibody specific for TADG-14, polyacrylamide gel electrophoresis, or HPLC analysis. A protein is substantially free of naturally associated components when it is separated from at least some of those contaminants which accompany it in its natural state. Thus, a protein which is chemically synthesized or produced in a cellular system different from the cell from which it naturally originates will

be, by definition, substantially free from its naturally associated components. Accordingly, substantially pure proteins include eukaryotic proteins synthesized in *E. coli*, other prokaryotes, or any other organism in which they do not naturally occur.

In addition to substantially full-length proteins, the invention also includes fragments (e.g., antigenic fragments) of the TADG-14 protein (SEQ ID No: 7). As used herein, "fragment," as applied to a polypeptide, will ordinarily be at least 10 residues, more typically at least 20 residues, and preferably at least 30 (e.g., 50) residues in length, but less than the entire, intact sequence. Fragments of the TADG-14 protein can be generated by methods known to those skilled in the art, e.g., by enzymatic digestion of naturally occurring or recombinant TADG-14 protein, by recombinant DNA techniques using an expression vector that encodes a defined fragment of TADG-14, or by chemical synthesis. The ability of a candidate fragment to exhibit a characteristic of TADG-14 (e.g., binding to an antibody specific for TADG-14) can be assessed by methods described herein. Purified TADG-14 or antigenic fragments of TADG-14 can be used to generate new antibodies or to test existing antibodies (e.g., as positive controls in a diagnostic assay) by employing standard protocols known to those skilled in the art. Included in this invention are polyclonal antisera generated by using TADG-14 or a fragment of TADG-14 as the immunogen in, e.g., rabbits. Standard protocols for monoclonal and polyclonal antibody production known to those skilled in this art are

employed. The monoclonal antibodies generated by this procedure can be screened for the ability to identify recombinant TADG-14 cDNA clones, and to distinguish them from known cDNA clones.

Further included in this invention are TADG-14 proteins which are encoded at least in part by portions of SEQ ID NO: 7, e.g., products of alternative mRNA splicing or alternative protein processing events, or in which a section of TADG-14 sequence has been deleted. The fragment, or the intact TADG-14 polypeptide, may be covalently linked to another polypeptide, e.g. which acts as a label, a ligand or a means to increase antigenicity.

The invention also includes a polyclonal or monoclonal antibody which specifically binds to TADG-14. The invention encompasses not only an intact monoclonal antibody, but also an immunologically-active antibody fragment, e.g., a Fab or $(Fab)_2$ fragment; an engineered single chain Fv molecule; or a chimeric molecule, e.g., an antibody which contains the binding specificity of one antibody, e.g., of murine origin, and the remaining portions of another antibody, e.g., of human origin.

In one embodiment, the antibody, or a fragment thereof, may be linked to a toxin or to a detectable label, e.g. a radioactive label, non-radioactive isotopic label, fluorescent label, chemiluminescent label, paramagnetic label, enzyme label, or colorimetric label. Examples of suitable toxins include diphtheria toxin, *Pseudomonas* exotoxin A, ricin, and cholera toxin. Examples of suitable enzyme labels include malate hydrogenase,

staphylococcal nuclease, delta-5-steroid isomerase, alcohol dehydrogenase, alpha-glycerol phosphate dehydrogenase, triose phosphate isomerase, peroxidase, alkaline phosphatase, asparaginase, glucose oxidase, beta-galactosidase, ribonuclease, urease, catalase, glucose-6-phosphate dehydrogenase, glucoamylase, acetylcholinesterase, etc. Examples of suitable radioisotopic labels include ^{3}H, ^{125}I, ^{131}I, ^{32}P, ^{35}S, ^{14}C, etc.

Paramagnetic isotopes for purposes of *in vivo* diagnosis can also be used according to the methods of this invention. There are numerous examples of elements that are useful in magnetic resonance imaging. For discussions on *in vivo* nuclear magnetic resonance imaging, see, for example, Schaefer et al., (1989) *JACC* 14, 472-480; Shreve et al., (1986) *Magn. Reson. Med.* 3, 336-340; Wolf, G. L., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 93-95; Wesbey et al., (1984) *Physiol. Chem. Phys. Med. NMR* 16, 145-155; Runge et al., (1984) *Invest. Radiol.* 19, 408-415. Examples of suitable fluorescent labels include a fluorescein label, an isothiocyalate label, a rhodamine label, a phycoerythrin label, a phycocyanin label, an allophycocyanin label, an ophthaldehyde label, a fluorescamine label, etc. Examples of chemiluminescent labels include a luminal label, an isoluminal label, an aromatic acridinium ester label, an imidazole label, an acridinium salt label, an oxalate ester label, a luciferin label, a luciferase label, an aequorin label, etc.

Those of ordinary skill in the art will know of other suitable labels which may be employed in accordance with the

present invention. The binding of these labels to antibodies or fragments thereof can be accomplished using standard techniques commonly known to those of ordinary skill in the art. Typical techniques are described by Kennedy et al., (1976) *Clin. Chim. Acta* 70, 1-31; and Schurs et al., (1977) *Clin. Chim. Acta* 81, 1-40. Coupling techniques mentioned in the latter are the glutaraldehyde method, the periodate method, the dimaleimide method, the m-maleimidobenzyl-N-hydroxy-succinimide ester method. All of these methods are incorporated by reference herein.

Also within the invention is a method of detecting TADG-14 protein in a biological sample, which includes the steps of contacting the sample with the labelled antibody, e.g., radioactively tagged antibody specific for TADG-14, and determining whether the antibody binds to a component of the sample.

As described herein, the invention provides a number of diagnostic advantages and uses. For example, the TADG-14 protein is useful in diagnosing cancer in different tissues since this protein is absent in highly proliferating cells. Antibodies (or antigen-binding fragments thereof) which bind to an epitope specific for TADG-14, are useful in a method of detecting TADG-14 protein in a biological sample for diagnosis of cancerous or neoplastic transformation. This method includes the steps of obtaining a biological sample (e.g., cells, blood, plasma, tissue, etc.) from a patient suspected of having cancer, contacting the sample with a labelled antibody (e.g., radioactively tagged antibody) specific for

TADG-14, and detecting the TADG-14 protein using standard immunoassay techniques such as an ELISA. Antibody binding to the biological sample indicates that the sample contains a component which specifically binds to an epitope within TADG-14.

Likewise, a standard Northern blot assay can be used to ascertain the relative amounts of TADG-14 mRNA in a cell or tissue obtained from a patient suspected of having cancer, in accordance with conventional Northern hybridization techniques known to those persons of ordinary skill in the art. This Northern assay uses a hybridization probe, e.g. radiolabelled TADG-14 cDNA, either containing the full-length, single stranded DNA having a sequence complementary to SEQ ID NO: 6 (Figure 6), or a fragment of that DNA sequence at least 20 (preferably at least 30, more preferably at least 50, and most preferably at least 100 consecutive nucleotides in length). The DNA hybridization probe can be labelled by any of the many different methods known to those skilled in this art.

Antibodies to the TADG-14 protein can be used in an immunoassay to detect increased levels of TADG-14 protein expression in tissues suspected of neoplastic transformation. These same uses can be achieved with Northern blot assays and analyses.

The present invention is directed to DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of

(a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Preferably, the DNA has the sequence shown in SEQ ID No. 6. More preferably, the DNA encodes a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell. Preferably, the vector contains DNA encoding a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a host cell transfected with the vector described herein, said vector expressing a TADG-14 protein. Representative host cells include consisting of bacterial cells, mammalian cells and insect cells.

The present invention is also directed to a isolated and purified TADG-14 protein coded for by DNA selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Preferably, the isolated and purified TADG-14 protein of claim 9 having the amino acid sequence shown in SEQ ID No. 7.

The present invention is also directed to a method of detecting expression of the protein of claim 1, comprising the steps of: (a) contacting mRNA obtained from the cell with the labeled hybridization probe; and (b) detecting hybridization of the probe with the mRNA.

The following examples are given for the purpose of illustrating various embodiments of the invention and are not meant to limit the present invention in any fashion.

EXAMPLE 1

Tissue collection and storage

Upon patient hysterectomy, bilateral salpingo-oophorectomy, or surgical removal of neoplastic tissue, the specimen is retrieved and placed it on ice. The specimen was then taken to the resident pathologist for isolation and identification of specific tissue samples. Finally, the sample was frozen in liquid nitrogen, logged into the laboratory record and stored at -80°C. Additional specimens were frequently obtained from the Cooperative Human Tissue Network (CHTN). These samples were prepared by the CHTN and shipped to us on dry ice. Upon arrival, these specimens were logged into the laboratory record and stored at -80°C.

EXAMPLE 2

mRNA isolation and cDNA synthesis

Messenger RNA (mRNA) isolation was performed according to the manufacturer's instructions using the Mini RiboSepTM Ultra mRNA isolation kit purchased from Becton Dickinson (cat. # 30034). This was an oligo(dt) chromatography based system of mRNA isolation. The amount of mRNA recovered was quantitated by UV spectrophotometry.

First strand complementary DNA (cDNA) was synthesized using 5.0 mg of mRNA and either random hexamer or oligo(dT) primers according to the manufacturer's protocol utilizing a first strand synthesis kit obtained from Clontech (cat.# K1402-1). The purity of the cDNA was evaluated by PCR using primers specific for the p53 gene. These primers span an intron such that pure cDNA can be distinguished from cDNA that is contaminated with genomic DNA.

EXAMPLE 3

PCR reactions

Reactions were carried out as follows: first strand cDNA generated from 50 ng of mRNA will be used as template in the presence of 1.0 mM MgCl2, 0.2 mM dNTPs, 0.025 U Taq polymerase/ml of reaction, and 1x buffer supplied with enzyme. In addition, primers must be added to the PCR reaction. Degenerate

primers which may amplify a variety of cDNAs are used at a final concentration of 2.0 mM each, whereas primers which amplify specific cDNAs are added to a final concentration of 0.2 mM each.

After initial denaturation at 95°C for 3 minutes, thirty cycles of PCR are carried out in a Perkin Elmer Gene Amp 2400 thermal cycler. Each cycle consists of 30 seconds of denaturation at 95°C, 30 seconds of primer annealing at the appropriate annealing temperature*, and 30 seconds of extension at 72°C. The final cycle will be extended at 72°C for 7 minutes. To ensure that the reaction succeeded, a fraction of the mixture will be electrophoresed through a 2% agarose/TAE gel stained with ethidium bromide(final concentration 1 mg/ml). The annealing temperature varies according to the primers that are used in the PCR reaction. For the reactions involving degenerate primers, an annealing temperature of 48°C were used. The appropriate annealing temperature for the TADG14 and β-tubulin specific primers is 62°C.

EXAMPLE 4

T-vector ligation and transformations

The purified PCR products are ligated into the Promega T-vector plasmid and the ligation products are used to transform JM109 competent cells according to the manufacturer's instructions (Promega cat. #A3610). Positive colonies were cultured for amplification, the plasmid DNA isolated by means of the WizardTM

Minipreps DNA purification system (Promega cat #A7500), and the plasmids were digested with ApaI and SacI restriction enzymes to determine the size of the insert. Plasmids with inserts of the size(s) visualized by the previously described PCR product gel electrophoresis were sequenced.

EXAMPLE 5

DNA sequencing

Utilizing a plasmid specific primer near the cloning site, sequencing reactions were carried out using PRISMTM Ready Reaction Dye DeoxyTM terminators (Applied Biosystems cat# 401384) according to the manufacturer's instructions. Residual dye terminators were removed from the completed sequencing reaction using a Centri-sepTM spin column (Princeton Separation cat.# CS-901). An Applied Biosystems Model 373A DNA Sequencing System was available and was used for sequence analysis. Based upon the determined sequence, primers that specifically amplify the gene of interest were designed and synthesized.

EXAMPLE 6

Northern blot analysis

mRNAs (approximately 5 mg) were size separated by electrophoresis through a 6.3% formaldehyde, 1.2% agarose gel in

0.02 M MOPS, 0.05 M sodium acetate (pH 7.0), and 0.001 M EDTA. The mRNAs were then blotted to Hybond-N (Amersham) by capillary action in 20x SSPE. The RNAs are fixed to the membrane by baking for 2 hours at 80°C. Additional multiple tissue northern (MTN) blots were purchased from CLONTECH Laboratories, Inc. These blots include the Human MTN blot (cat.#7760-1), the Human MTN II blot (cat.#7759-1), the Human Fetal MTN II blot (cat.#7756-1), and the Human Brain MTN III blot (cat.#7750-1). The appropriate probes were radiolabelled utilizing the Prime-a-Gene Labelling System available from Promega (cat#U1100). The blots were probed and stripped according to the ExpressHyb Hybridization Solution protocol available from CLONTECH (cat.#8015-1 or 8015-2).

EXAMPLE 7

Quantitative PCR

Quantitative-PCR was performed in a reaction mixture consisting of cDNA derived from 50 ng of mRNA, 5 pmol of sense and antisense primers for TADG14 and the internal control β-tubulin, 0.2 mmol of dNTPs, 0.5 mCi of [α-32P]dCTP, and 0.625 U of Taq polymerase in 1x buffer in a final volume of 25 ml. This mixture was subjected to 1 minute of denaturation at 95°C followed by 30 cycles of denaturation for 30 seconds at 95°C, 30 seconds of annealing at 62°C, and 1 minute of extension at 72°C with an additional 7 minutes of extension on the last cycle. The product was electrophoresed through a 2% agarose gel for separation, the gel was

dried under vacuum and autoradiographed. The relative radioactivity of each band was determined by PhosphoImager from Molecular Dynamics.

EXAMPLE 8

The present invention describes the use of primers directed to conserved areas of the serine protease class to identify members of that class which are overexpressed in carcinoma. Several genes were identified and cloned in other tissues, but not previously associated with ovarian carcinoma. The present invention describes a novel protease identified in ovarian carcinoma. This gene was identified using primers to the conserved area surrounding the catalytic domain amino acid histidine and the catalytic domain amino acid serine which is about 150 amino acids downstream towards the carboxyl end.

The gene encoding the novel extracellular serine protease of the present invention was identified from a group of proteases overexpressed in carcinoma by subcloning and sequencing the appropriate PCR products. An example of such a PCR reaction is given in Figure 1. Subcloning and sequencing of individual bands from such an amplification provided a basis for identifying the novel protease of the present invention.

EXAMPLE 9

The sequence determined for the catalytic domain of TADG-14 is presented in Figure 2 and is consistent with other serine proteases and specifically contains conserved amino acids appropriate for the catalytic domain of the serine protease family. Specific primers (20mers) derived from this sequence were used.

A series of normal and tumors cDNAs were examined to determine the expression of the TADG-14 protein. In a series of three normals compared to nine carcinomas using β-tubulin as an internal control for PCR amplification, TADG-14 was significantly overexpressed in eight of the nine carcinomas and either was not detected or was detected at a very low level in normal epithelial tissue (Figure 3). This evaluation was extended to a standard panel of about 35 tumors. Using these specific primers, the expression of this gene was also examined in both tumor cell lines and other tumor tissues as shown in Figure 4. The expression of TADG-14 was also observed in breast carcinoma and colon carcinoma. TADG-14 expression was not noted in other tissues. For example, TADG-14 was not present in detectable levels by Northern blot analysis in any of the following normal tissues: fetal lung, fetal heart, fetal brain, fetal kidney, adult spleen, thymus, prostate, testis, ovary, small intestine, colon, peripheral blood leukocytes, heart, placenta, lung, liver, skeletal muscle, kidney, pancreas, amygdala, caudate nucleus,

corpus callosum, hippocampus, whole brain, substantia nigr, subthalamic nucleus and thalamus.

Using the specific sequence for TADG-14 covering the full domain of the catalytic site as a probe for Northern blot analysis, three Northern blots were examined: one derived from ovarian tissues, both normal and carcinoma; one from fetal tissues; and one from adult normal tissues. As noted in Figure 5, abundant transcripts for TADG-14 were noted in ovarian carcinomas. Transcripts were noted in all carcinomas, but at lower levels in some sub-types of ovarian cancer. Furthermore, no transcript was observed from normal ovarian tissue. The transcript size was found to be approximately 1.4 kb. Of particular note is the fact that in the fetal tissue examined including brain, lung, liver, kidney and in multiple adult tissues examined, none of these blots showed expression for the TADG-14 transcript. The hybridization for the fetal and adult blots was appropriate and done with the same probe as with the ovarian tissue. Subsequent to this examination, it was confirmed that these blots contained other detectible mRNA transcripts

Using the base sequence derived from the original full length PCR clone corresponding to nucleotides 713-1160 of the catalytic domain as a probe to screen libraries, an ovarian carcinoma library derived from ascites tumor cells was examined for the presence of TADG-14. Four clones were obtained, two of which covered the complete mRNA 1.4kb transcript of the TADG-14 gene.

The complete nucleotide sequence (SEQ ID No:6) is provided in Figure 6 along with translation of the open reading frame (SEQ ID No:7).

In the nucleotide sequence, there is a Kozak sequence typical of sequences upstream from the initiation site of translation. There is also a polyadenylation signal sequence and a poly-A tail. The open reading frame consists of a 260 amino acid sequence (SEQ ID No:7) which includes a secretion signal sequence in the first 25 amino acids confirming the extracellular processing of the protease. Also a clear delineation of the catalytic domain conserved histidine, aspartic acid, serine series along with a series of amino acids conserved in the serine protease family is indicated.

Examination of the databases for both the expressed tag sequence and complete transcripts provided seven genes that had significant homology to this newly identified serine protease. One gene was identified from mouse brain and a comparison of the nucleotide homology is provided in Figure 7. A comparison of the homology of the amino acid sequence is provided in Figure 8. Alignment of TADG-14 with mouse neuropsin revealed 77.2% similarity and 72.2% identity at the amino acid levels for these two genes. Given that the size of the mouse transcript is 1.4kb and that the mouse gene contains 260 amino acids and there is greater than 70% homology, this gene may be a human equivalent of the mouse neuropsin gene or a family member of neuropsin-like genes.

TADG-14 is secreted and expressed early in tumor development and has invasive capacity. TADG-14 therefore is a

potential diagnostic for ovarian and other cancers. TADG-14 also may be a target for intervention in regulating tumor spread by inhibition, gene therapy, antibody inactivation technology. In addition to its obvious usefulness in ovarian carcinoma and other carcinomas including the preliminary data on breast and prostate, the neuropsin-like qualities may provide an opportunity for usefulness in neuropathologic disorders.

Any patents or publications mentioned in this specification are indicative of the levels of those skilled in the art to which the invention pertains. These patents and publications are herein incorporated by reference to the same extent as if each individual publication was specifically and individually indicated to be incorporated by reference.

One skilled in the art will readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The present examples along with the methods, procedures, treatments, molecules, and specific compounds described herein are presently representative of preferred embodiments, are exemplary, and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art which are encompassed within the spirit of the invention as defined by the scope of the claims.

WHAT IS CLAIMED IS:

1. DNA encoding a TADG-14 protein selected from the group consisting of:

(a) isolated DNA which encodes a TADG-14 protein;

(b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and

(c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

2. The DNA of claim 1, wherein said DNA has the sequence shown in SEQ ID No. 6.

3. The DNA of claim 1, wherein said TADG-14 protein has the amino acid sequence shown in SEQ ID No. 7.

4. A vector capable of expressing the DNA of claim 1 adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

5. The vector of claim 4, wherein said DNA encodes a TADG-14 protein having the amino acid sequence shown in SEQ ID No. 7.

6. A host cell transfected with the vector of claim 4, said vector expressing a TADG-14 protein.

7. The host cell of claim 6, wherein said cell is selected from group consisting of bacterial cells, mammalian cells, plant cells and insect cells.

8. The host cell of claim 7, wherein said bacterial cell is *E. coli*.

9. Isolated and purified TADG-14 protein coded for by DNA selected from the group consisting of:

(a) isolated DNA which encodes a TADG-14 protein;

(b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and

(c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein.

10. The isolated and purified TADG-14 protein of claim 9 having the amino acid sequence shown in SEQ ID No. 7.

11. A method of detecting expression of the protein of claim 1, comprising the steps of:

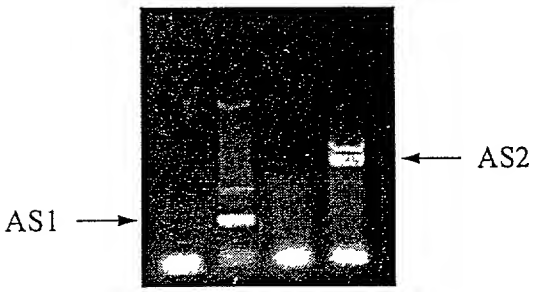
(a) contacting mRNA obtained from the cell with the labeled hybridization probe; and

(b) detecting hybridization of the probe with the mRNA.

ABSTRACT OF THE DISCLOSURE

The present invention provides a DNA encoding a TADG-14 protein selected from the group consisting of: (a) isolated DNA which encodes a TADG-14 protein; (b) isolated DNA which hybridizes to isolated DNA of (a) above and which encodes a TADG-14 protein; and (c) isolated DNA differing from the isolated DNAs of (a) and (b) above in codon sequence due to the degeneracy of the genetic code, and which encodes a TADG-14 protein. Also provided is a vector capable of expressing the DNA of the present invention adapted for expression in a recombinant cell and regulatory elements necessary for expression of the DNA in the cell.

SERINE PROTEASE PRIMERS



1) Normal Ovary 2) Tumor
3) Normal Ovary 4) Tumor

Figure 1 shows a comparison of PCR products derived from normal and carcinoma cDNA as shown by staining in an agarose gel. Two distinct bands (lane 2) were present in the primer pair sense-His-antisense ASP-(AS1) and multiple bands of about 500 bp are noted in the carcinoma lane for the sense-His antisense-SER (AS2) primer pairs (lane 4).

primer

```
201                                                        250
  Prom  WVLTAAHCKK PNLQV....F LGKHNLRQRE SSQEQSSVVR AVIHPDY...  SEQ ID No:1
Tadg14  WVVTAAHCKK PKYTV....R LGDHSLQNKD GPEQEIPVVQ SIPHPCY...  SEQ ID No:2
  Tryl  WVVSAGHCYK SRIQV....R LGEHNIEVLE GNEQFINAAK IIRHPQY...  SEQ ID No:3
  Scce  WVLTAAHCKM NEYTV....H LGSDTLGDRR A..QRIKASK SFRHPGY...  SEQ ID No:4
  Heps  WVLTAAHCFP ERNRVLSRWR VFAGAVAQAS PHGLQLGVQA VVYHGGYLPF  SEQ ID No:5

        251                                                300
  Prom  ...DAASHDQ DIMLLRLARP AKLSELIQPL PLERDCSA.. NTTSCHILGW
Tadg14  NSSDVEDHNH DLMLLQLRDQ ASLGSKVKPI SLADHCTQ.. PGQNCTVSGW
  Tryl  ...DRKTLNN DIMLIKLSSR AVINARVSTI SLPTAPPA.. TGTKCLISGW
  Scce  ST...QTHVN DLMLVKLNSQ ARLSSMVKKV RLPSRCEP.. PGTTCTVSGW
  Heps  RDPNSEENSN DIALVHLSSP LPLTEYIQPV CLPAAGQALV DGKICTVTGW

        301                                                350
  Prom  GKTAD..GDF PDTIQCAYIH LVSREECEHA ..YPGQITQN MLCAGDEKYG
Tadg14  GTVTSPRENF PDTLNCAEVK IFPQKKCEDA ..YPGQITDG MVCAGSSK.G
  Tryl  GNTASSGADY PDELQCLDAP VLSQAKCEAS ..YPGKITSN MFCVGFLEGG
  Scce  GTTTSPDVTF PSDLMCVDVK LISPQDCTKV ..YKDLLENS MLCAGIPDSK
  Heps  GNTQYYGQQ. AGVLQEARVP IISNDVCNGA DFYGNQIKPK MFCAGYPEGG

        351
  Prom  KDSCQGDSGG
Tadg14  ADTCQGDSGG
  Tryl  KDSCQGDSGG
  Scce  KNACNGDSGG
  Heps  IDACQGDSGG
```

primer

Figure 2. Comparison of amino acid sequence of TADG-14 with known serine protease catalytic domains.

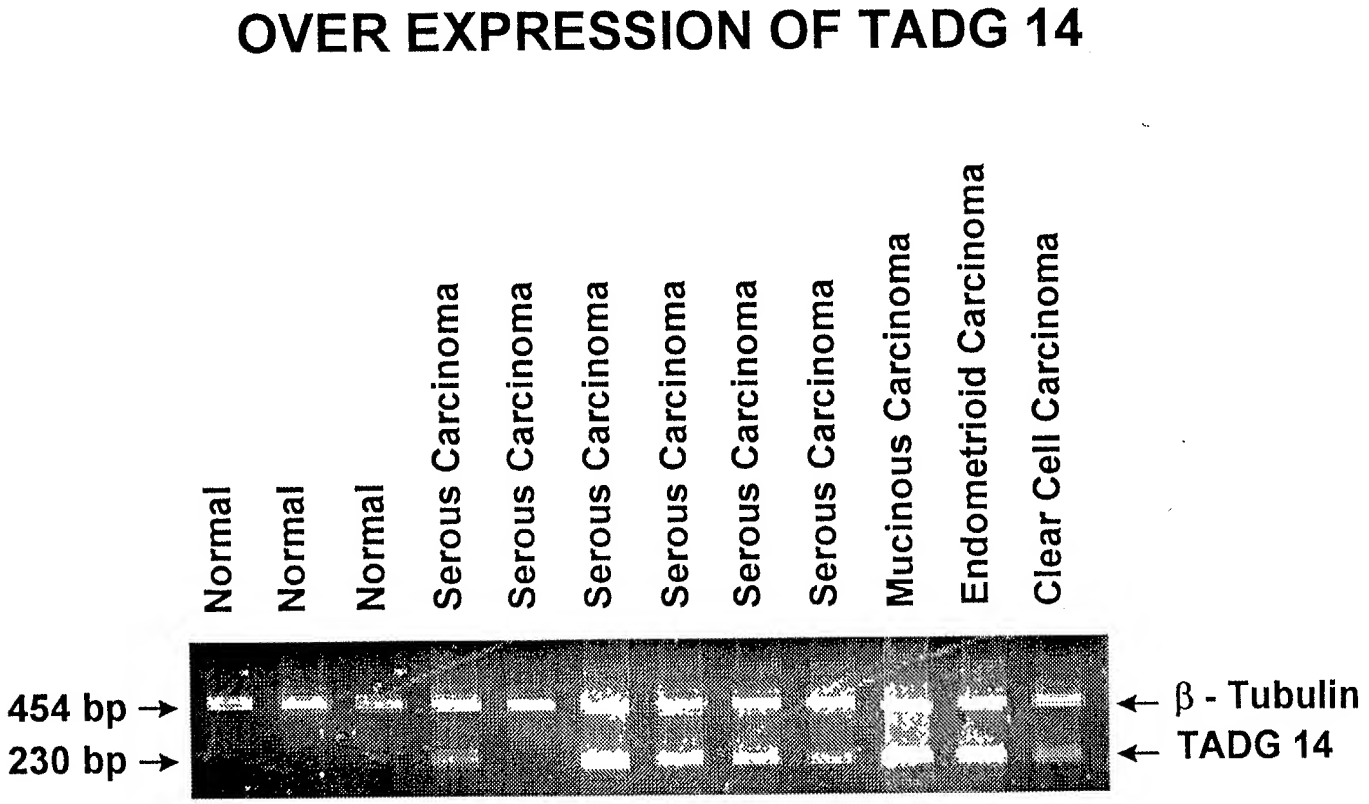


Figure 3. Overexpression of TADG-14 in ovarian carcinomas.

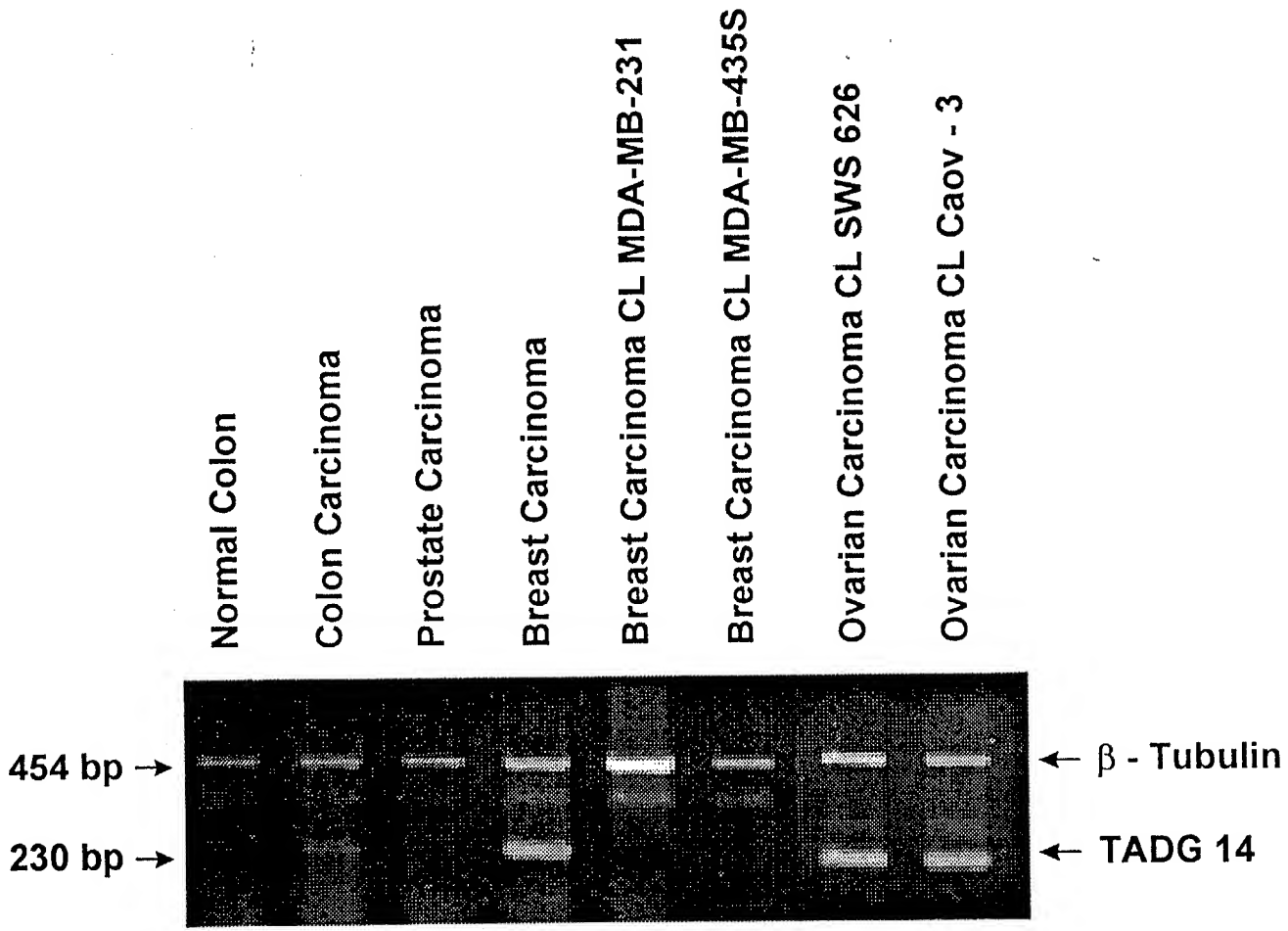


Figure 4. TADG-14 expression in tumors and cell lines.

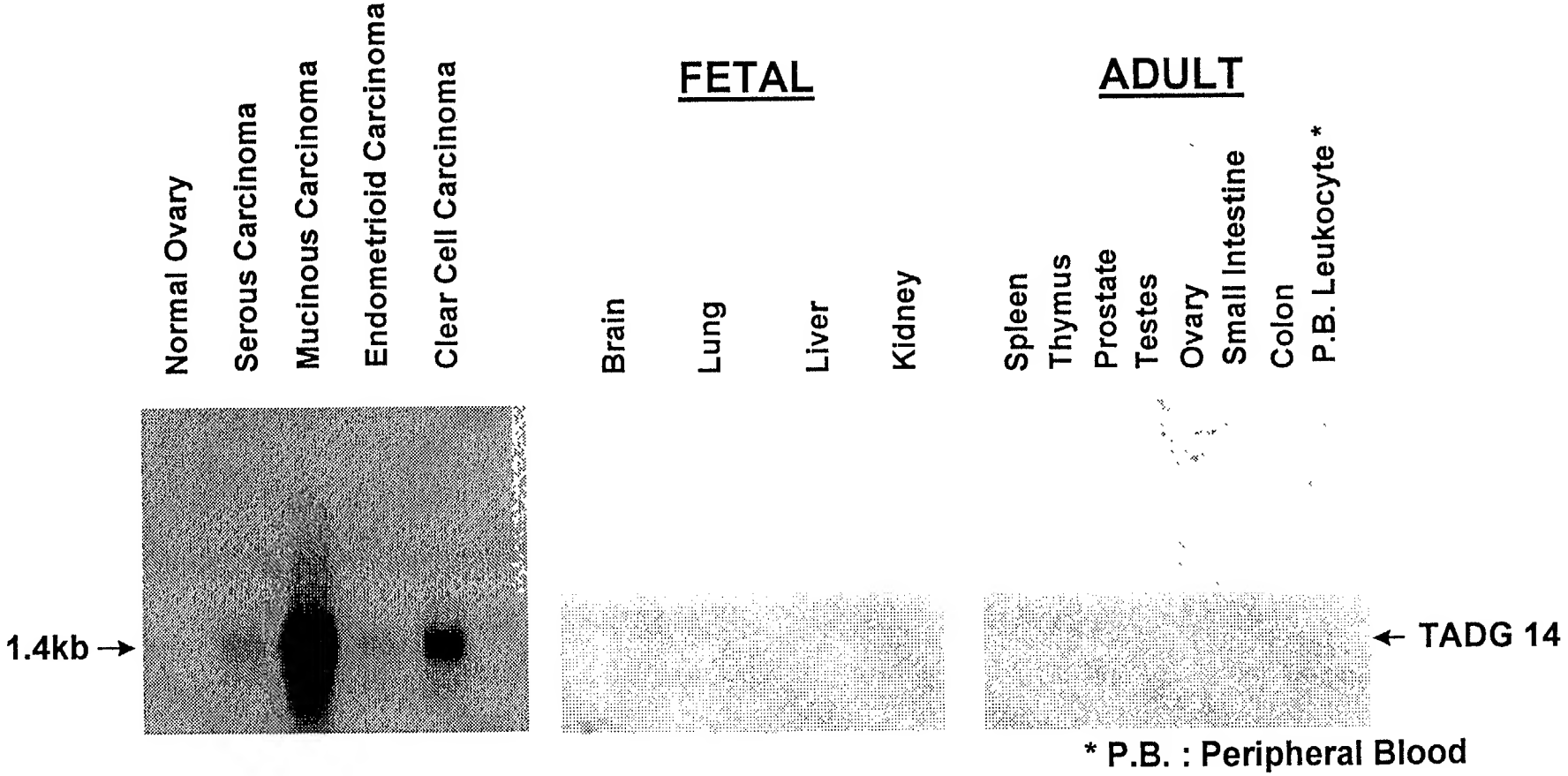
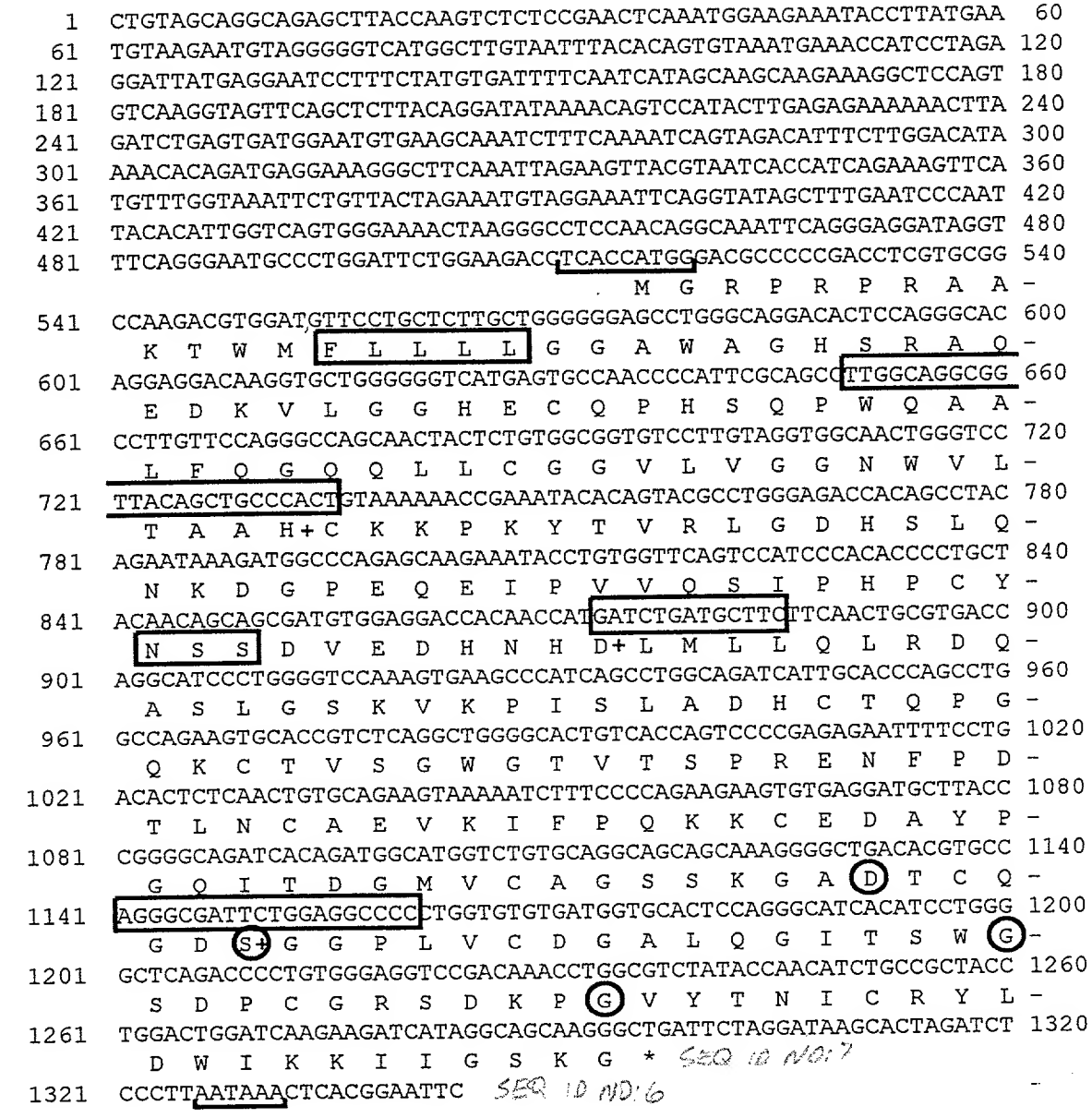


Figure 5. Blots: TADG-14 expression in fetal, adult and ovarian carcinoma tissues.



= Kozak's Consensus sequence

+ = Conserved amino acids of catalytic triad H, D, S

NSS = Possible N - linked glycosylation site

= Poly - adenylation signal

= Conserved nt of catalytic triad

= aa required for formation of an oxyanion hole for catalytic activity

FLLL = Secretion signal sequence

Figure 6. Complete sequence of TADG-14 transcript including ORF and common domains.

Figure 7. Homology of TADG-14 with mouse neuropsin. 76% identity for ORF. Low homology outside of ORF.

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T14   506 AGACCTCACCATGGGACGCCCCCGACCTCGTGCGGCCAAGACGTGGATGT 555

                    .         .         .         .         .
          527 TTCTGCTTCTGTTCATGGGAGCGTGGGCAGGGCTCACCAGAGCTCAGGGC 576
              | |||||  || |   |||||| |||||||| | | |||| || ||||
          556 TCCTGCTCTTGCTGGGGGGAGCCTGGGCAGGACACTCCAGGGCACAGGAG 605

                    .         .         .         .         .
          577 TCCAAGATCCTGGAAGGTCGAGAGTGTATACCCCACTCCCAGCCTTGGCA 626
                |||| | ||||  ||||  |||||   |||||| || ||||||||||||
          606 GACAAGGTGCTGGGGGGTCATGAGTGCCAACCCCATTCGCAGCCTTGGCA 655

                    .         .         .         .         .
          627 GGCAGCCTTGTTCCAGGGCGAGAGACTGATCTGTGGGGGTGTCCTGGTTG 676
              ||| |||||||||||||||  ||  |||  ||||||| |||||||| || |
          656 GGCGGCCTTGTTCCAGGGCCAGCAACTACTCTGTGGCGGTGTCCTTGTAG 705

                    .         .         .         .         .
          677 GAGACAGATGGGTCCTCACGGCAGCCCACTGCAAAAAACAGAAGTACTCC 726
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          706 GTGGCAACTGGGTCCTTACAGCTGCCCACTGTAAAAAACCGAAATACACA 755

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          727 GTGCGTCTGGGTGATCATAGCCTCCAGAGCAGAGATCAGCCGGAGCAGGA 776
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                    .         .         .         .         .
          777 GATCCAGGTGGCTCAGTCTATCCAGCATCCTTGCTACAACAACAGCAACC 826
               || |  |||| |||||| ||||  || || |||||||||| |||| |
          806 AATACCTGTGGTTCAGTCCATCCCACACCCCTGCTACAACAGCAGCGATG 855

                    .         .         .         .         .
          827 CAGAAGATCACAGTCACGATATAATGCTCATTCGACTGCAGAACTCAGCA 876
                || || ||||  || ||| | |||||  ||| |||||   ||   |||
          856 TGGAGGACCACAACCATGATCTGATGCTTCTTCAACTGCGTGACCAGGCA 905

                    .         .         .         .         .
          877 AACCTCGGGGACAAGGTGAAGCCGGTCCAACTGGCCAATCTGTGTCCCAA 926
              |||  |||  ||| |||||||||  ||   |||||  |||  ||  || |
          906 TCCCTGGGGTCCAAAGTGAAGCCCATCAGCCTGGCAGATCATTGCACCCA 955

                    .         .         .         .         .
          927 AGTTGGCCAGAAGTGCATCATATCAGGCTGGGGCACTGTCACCAGCCCTC 976
              |||||||||||||||  | | ||||||||||||||||||||||||| || |
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                    .         .         .         .         .
          977 AAGAGAACTTTCCAAACACCCTCAACTGTGCGGAAGTGAAAATCTATTCC 1026
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                .         .         .         .         .
1027 CAGAACAAGTGTGAGAGAGCCTATCCAGGGAAGATCACCGAGGGCATGGT 1076
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1056 CAGAAGAAGTGTGAGGATGCTTACCCGGGGCAGATCACAGATGGCATGGT 1105
                .         .         .         .         .
1077 CTGTGCTGGCAGCAGCAATGGAGCTGACACGTGCCAGGGTGACTCAGGAG 1126
     |||||| ||||||||||| || |||||||||||||||| || || ||||
1106 CTGTGCAGGCAGCAGCAAAGGGGCTGACACGTGCCAGGGCGATTCTGGAG 1155
                .         .         .         .         .
1127 GCCCTCTGGTGTGCGACGGGATGCTCCAGGGCATCACCTCATGGGGCTCA 1176
     |||| |||||||| || ||    |||||||||||||| || |||||||||
1156 GCCCCCTGGTGTGTGATGGTGCACTCCAGGGCATCACATCCTGGGGCTCA 1205
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1177 GACCCCTGTGGGAAACCCGAGAAACCTGGAGTCTACACCAAAATCTGCCG 1226
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1206 GACCCCTGTGGGAGGTCCGACAAACCTGGCGTCTATACCAACATCTGCCG 1255
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1227 CTACACTACCTGGATCAAGAAGACCATGGACAACAGGGACTGATCCTGG 1275
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          |||| | | .|. |||  ||||| .|||  |:| | || ||||||||||
Neurop  1 MGRPPPCAIQPWILLLLFMGAWAGLTRAQGSKILEGRECIPHSQPWQAAL 50
                    .         .         .         .         .
         51 FQGQQLLCGGVLVGGNWVLTAAHCKKPKYTVRLGDHSLQNKDGPEQEIPV 100
            |||:.|:|||||||  |||||||||| ||.|||||||||.:| ||||| |
         51 FQGERLICGGVLVGDRWVLTAAHCKKQKYSVRLGDHSLQSRDQPEQEIQV 100
                    .         .         .         .         .
        101 VQSIPHPCYNSSDVEDHNHDLMLLQLRDQASLGSKVKPISLADHCTQPGQ 150
             ||| |||||.|. |||.||:||:.|.. |.|| ||||: ||. | . ||
        101 AQSIQHPCYNNSNPEDHSHDIMLIRLQNSANLGDKVKPVQLANLCPKVGQ 150
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        151 KCTVSGWGTVTSPRENFPDTLNCAEVKIFPQKKCEDAYPGQITDGMVCAG 200
            || :||||||||||.||||.||||||||||: | ||| ||||.||:||||||
        151 KCIISGWGTVTSPQENFPNTLNCAEVKIYSQNKCERAYPGKITEGMVCAG 200
                    .         .         .         .         .
        201 SSKGADTCQGDSGGPLVCDGALQGITSWGSDPCGRSDKPGVYTNICRYLD 250
            || |||||||||||||||| ||||||||||||: :|||||| ||||
        201 SSNGADTCQGDSGGPLVCDGMLQGITSWGSDPCGKPEKPGVYTKICRYTT 250

        251 WIKKIIGSKG 260
            |||| . .:
        251 WIKKTMDNRD 260
```

Figure 8. Amino acid homology of TADG-14 with mouse neuropsin.

DOCKET NO: D6020

COMBINED DECLARATION AND POWER OF ATTORNEY

I, **TIMOTHY J. O'BRIEN,** hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, I believe I am the original, first and co-inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled, **NOVEL EXTRACELLULAR SERINE PROTEASE** the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56(a).

I hereby appoint the following attorneys and/or agents to prosecute this application and to transact all business in the Patent and Trademark Office connected therewith: Dr. Benjamin Adler, Registration No. 35,423 and Sarah J. Brashears, Registration No. 38,087. Address all telephone calls to Dr. Benjamin Adler at telephone number 713/777-2321. Address all correspondence to Dr. Benjamin Adler, McGREGOR & ADLER, P.C., 8011 Candle Lane, Houston, TX 77071.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patents issued thereon.

Full Name of Inventor: TIMOTHY J. O'BRIEN

Inventor's Signature: Timothy J O'Brien Date: 8/20/97

Residence Address: 2625 Grist Mill Rd., Little Rock, AR 72227

Citizen of: United States of America

Post Office Address: 2625 Grist Mill Rd., Little Rock, AR 72227

DOCKET NO: D6020

COMBINED DECLARATION AND POWER OF ATTORNEY

I, **LOWELL J. UNDERWOOD,** hereby declare that:

My residence, post office address and citizenship are as stated below next to my name, I believe I am the original, first and co-inventor of the subject matter which is claimed and for which a patent is sought on the invention entitled, **NOVEL EXTRACELLULAR SERINE PROTEASE** the specification of which is attached hereto.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above. I acknowledge the duty to disclose all information I know to be material to patentability in accordance with Title 37, Code of Federal Regulations, §1.56(a).

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Full Name of Inventor: LOWELL J. UNDERWOOD

Inventor's Signature: _____ Date: 8-20-97

Residence Address: 121 N. Jackson St. Apt. K Little Rock, Arkansas 72205

Citizen of: United States of America

Post Office Address: Little Rock, Arkansas 72205

Applicant or Patentee: O'Brien, *et al.* Attorney's Docket No.: D6020
Serial or Patent No.:
Filed or Issued:
For: ***Novel Extracellular Serine Protease***

VERIFIED STATEMENT (DECLARATION) CLAIMING SMALL ENTITY STATUS (37 CFR 1.9(f) and 1.27(c)) - NONPROFIT ORGANIZATION

I hereby declare that I am an official of the nonprofit organization empowered to act on behalf of the concern identified below:

Name Of Organization: **Board of Trustees of the University of Arkansas**
Address Of Concern: **1123 S. University Ave., Suite 601**
Little Rock, Arkansas 72204

Type Of Organization: **X** - University of other institution of higher learning

I hereby declare that the above identified nonprofit organization qualifies as a nonprofit organization as defined in 37 CFR 1.9(e), for purposes of paying reduced fees under section 41(a) and (b) of Title 35, United States Code.

I hereby declare that rights under contract or law have been conveyed to and remain with the nonprofit organization identified above with regard to the invention, entitled: ***Novel Extracellular Serine Protease*** by inventor(s) **O'Brien, *et al.*** described in the specification filed herewith.

If the rights held by the above identified nonprofit organization are not exclusive, each individual, concern or organization having rights to the invention is listed below* and no rights to the invention are held by any person, other than the inventor, who could not qualify as a small business concern under 37 CFR 1.9(d) or by any concern which would not qualify as a small business concern under 37 CFR .9(d) or a nonprofit organization under 37 CFR 1.9(e).

*NOTE: Separate verified statements are required from each named person, concern or organization having rights to the invention averring to their status as small entities. (37 CFR 1.27)

Name _____
Address _____
[ ]Individual [ ] Small Business Concern [X]Nonprofit Organization

I acknowledge the duty to file, in this application or patent, notification of any change in status resulting in loss of entitlement to small entity status prior to paying, or at the time of paying, the earliest of the issue fee or any maintenance fee due after the date on which status as a small entity is no longer appropriate. (37 CFR 1.28(b))

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application, any patent issuing thereon, or any patent to which this verified statement is directed.

Name Of Person Signing Harold J. Evans, Esq.
Title Of Person Other Than Owner Associate VP for Legal Affairs
Address Of Person Signing _____
University of Arkansas
1123 S. University, Suite 601
Little Rock, AR 72204
Signature _____
Date August 19, 1997